

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of James T. English, et al.

Art Unit 1639

Serial No. 09/829,549

Filed April 10, 2001

Confirmation No. 8198

For PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES

Examiner Teresa D. Wessendorf

SECOND AMENDED APPEAL BRIEF

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Examiner Teresa D. Wessendorf

January 18, 2007

SECOND AMENDED APPEAL BRIEF

This is an appeal from the final rejection of the claims of the above-referenced application made in the Office action dated July 25, 2005. A Notice of Appeal was filed on December 22, 2005.

This Second Amended Appeal Brief is being submitted in response to the Notification of Non-Compliant Appeal Brief dated December 19, 2006. In that Notification, the Office asserts that the Appellants' First Amended Appeal Brief is defective because it failed to respond to every ground of rejection presented for review. According to the Office,

Appellants' brief is not responsive to every ground of rejection given by the examiner for dependent claims 5, 35-36, 38 and etc. (See Office action mailed on 2/9/2005). While the Final Office action mailed on 7/25/2005 did not contain the headings for the rejections of the dependent claims, however, it is evident from the action that the rejections had been maintained. (See e.g., page 12 of the 7/25/05 Office action).

With due respect, it is believed that the Office is in error. In the final rejection, the Office only recited one ground of rejection and Appellants fully addressed this rejection in their Pre-Appeal Brief Request for Review, Appeal Brief, and First Amended Appeal Brief.¹

According to 37 C.F.R. 1.113, in a final Office action, the Office shall repeat each applicable ground of rejection:

¹ Appellants note that their originally filed Appeal Brief dated June 6, 2006, was not found to be defective for failing to include each ground of rejection in the Notice of Non-Compliant Appeal Brief dated August 24, 2006.

(a) On the second or any subsequent examination or consideration by the examiner the rejection or other action may be made final,

(b) In making such final rejection, *the examiner **shall repeat or state all grounds of rejection then considered applicable** to the claims of the application, clearly stating the reasons in support thereof.*²

The mandatory nature of this requirement is reflected in the Manual of Patent

Examining Procedure (M.P.E.P.):

STATEMENT OF GROUNDS

In making the final rejection, *all outstanding grounds of rejection of record should be carefully reviewed, **and any such grounds relied on in the final rejection should be reiterated.***³

By failing to comply with the C.F.R. and the M.P.E.P., the Office has failed to preserve any and all grounds of rejection not included in the final Office action. The Office so much as admits these omissions in the Notification of Non-Compliant Appeal Brief dated December 19, 2006, and then attempts to recover them by stating that it was “evident” from the final Office action that they were maintained

In the interest of economy, Appellants nonetheless include in this Second Amended Appeal Brief headings and arguments directed to the grounds of rejection which were omitted and thereby not maintained in the final rejection. In light of the foregoing, however, Appellants believe them to be unnecessary and that this appeal should be properly decided solely upon the issues, headings, groupings, and arguments presented in Appellants' First Amended Appeal Brief.

I. REAL PARTY IN INTEREST

The real party in interest is The Curators of the University of Missouri, a corporation of the state of Missouri. An assignment of the above-identified application from the inventors to The Curators of the University of Missouri is recorded in the U.S. Patent and Trademark Office at Reel 011962, Frame 0536.

² 37 C.F.R. 1.113(a) and (b) (emphasis added).

³ M.P.E.P. § 706.07 (emphasis added).

II. RELATED APPEALS AND INTERFERENCES

Appellants are unaware of any pending appeals or interferences which may be related to, directly affect or be affected by, or have a bearing on, the Board's decision in the present appeal.

III. STATUS OF CLAIMS

The following is a statement of the status of all claims:

Claims 1-9: Rejected under 35 U.S.C. § 103(a).

Claims 10-31: Cancelled.

Claims 32-51: Rejected under 35 U.S.C. § 103(a).

Thus, claims 1-9 and 32-51 stand rejected under 35 U.S.C. § 103(a). The rejection of claims 1-9 and 32-51 under 35 U.S.C. § 103(a) is being appealed.

IV. STATUS OF AMENDMENTS

No amendments have been filed after the final rejection.

V. SUMMARY OF CLAIMED SUBJECT MATTER

The following summary is a concise explanation of the subject matter defined in each of the independent claims (1, 48, and 49) involved in the appeal, referring to the specification by page and line number.⁴ This summary correlates claim elements to specific embodiments, but does not in any manner limit claim interpretation. Rather, the summary is provided only to facilitate the Board's understanding of the subject matter of this appeal.

Phytophthora is a disease-causing organism causing large losses in many agronomically important crop species. Control of these pathogens is particularly

⁴ Independent claims 1 and 49 (and dependent claims 2-4, 6-8, 32-34, 37-40, 45-47, and 50-51) are grouped together for purposes of this appeal. See Section VII(A)(1), *supra*.

difficult, and often requires the treatment of entire fields with biocidal compounds. While such methods are generally effective, increasing concern about the environment and economic costs of such treatments require the need for alternative control methods. The claimed invention provides a solution to this problem: the use of random peptide display to identify peptides that bind to pathogenic fungi of the genus *Phytophthora* and other pathogenic fungi.⁵

More specifically, the present invention provides a method for identifying non-immunoglobulin peptides having an affinity for the surface of a plant pathogen. The method of independent claim 1, for instance, comprises:

(a) constructing a library of peptides by (i) preparing random oligonucleotides, (ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell, and (iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector;⁶

(b) contacting a vector expressing the peptide library with a target fungus and removing unbound vector;⁷

(c) eluting bound vector from said fungus;⁸

(d) amplifying the bound vector;⁹

(e) sequencing the oligonucleotides contained in said eluted vector;¹⁰

(f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector;¹¹ and

(g) selecting the non-immunoglobulin peptides for which the amino acid sequence has been deduced.¹²

⁵ See Appellants' Specification, page 1, lines 14-15 and 18-21; and page 4, line 34 to page 5, line 4.

⁶ See Appellants' Specification, page 10, line 5 to page 12, line 7.

⁷ See Appellants' Specification, page 12, lines 8-24; see also page 21, line 25 to page 22, line 15 (Example 3).

⁸ See Appellants' Specification, page 12, lines 24-28; see also page 21, line 25 to page 22, line 15 (Example 3).

⁹ See Appellants' Specification, page 17, line 29 to page 13, line 9; see also page 22, lines 16-28 (Example 4).

¹⁰ See Appellants' Specification, page 13, lines 9-16; see also page 22, line 29 to page 23, line 19 (Example 5).

¹¹ *Id.*

¹² See Appellants' Specification, page 13, line 17 to page 14, line 9; see also page 22, line 29 to page 23, line 19 (Example 5); page 23, line 20 to page 24, line 16 (Example 6); and Figs. 2 and 3.

Independent claim 48 is similar to independent claim 1 and requires that the target fungus be selected from the group consisting of *Phytophthora sojae*,¹³ *Phytophthora capsici*,¹⁴ *Phytophthora palmivora*,¹⁵ *Phytophthora cinnamomi*,¹⁶ and *Phytophthora parasitica*.¹⁷

Independent claim 49 is similar to independent claim 1 and requires that the library of peptides be (1) an f8-1 peptide library, wherein each peptide of the f8-1 peptide library has a length of 8 amino acids¹⁸ or (2) an f88-4 peptide library, wherein each peptide of the f88-4 peptide library has a length of 15 amino acids¹⁹.

Claim 5, which depends from claims 1 or 48, requires that the sequence of the random oligonucleotides be GCA GNN (NNN)₇ or SEQ ID NO: 1.²⁰

Claim 9, which depends from claims 1 or 48, requires that each of the peptides be the same length, the length being 6 to 15 amino acids.²¹

Claim 35, which depends from claims 1 or 49, requires that the target fungus be selected from the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, and *Phytophthora parasitica*.²²

Claim 36, which depends from claims 1 or 49, requires that the target fungus be *Phytophthora sojae* or *Phytophthora capsici*.²³

Claim 44, which depends from claims 1 or 49, requires that the peptide library be an f88-4 peptide library.²⁴

Practically speaking, the library of peptides can be displayed on a vector such as phage and incubated with fungi of the genus *Phytophthora* to select for binding peptides. As described in Example 3, the f8-1 or the f88-4 phage-displayed peptide library can be incubated with *Phytophthora* zoospores at room temperature with gentle

¹³ See Appellants' Specification, page 20, lines 12-29 (Example 1).

¹⁴ *Id.*

¹⁵ See Appellants' Specification, page 2, line 12.

¹⁶ See Appellants' Specification, page 2, line 33.

¹⁷ See Appellants' Specification, page 20, lines 12-29 (Example 1).

¹⁸ See Appellants' Specification, page 11, lines 12-14; lines 16-19; and lines 20-27.

¹⁹ See Appellants' Specification, page 11, lines 14-16; and page 11, line 28 to page 12, line 8.

²⁰ See Appellants' Specification, page 11, line 20 to page 12, line 7.

²¹ See Appellants' Specification, page 10, lines 5-7. Dependent claims 9 and 41-43 are grouped together for purposes of this appeal. See Section VII(A)(2), *supra*.

²² See *supra*, notes 13 to 17.

²³ See *supra*, notes 13 and 14.

²⁴ See Appellants' Specification, page 11, lines 14-16.

agitation. Bound phage can then be eluted from the multitude of unknown epitopes on the *Phytophthora* zoospores with an elution buffer and purified. As described in Example 5, DNA can be isolated from phage clones that bound to the *Phytophthora* zoospores and sequenced to determine the peptide sequence that the DNA encodes.

After the binding peptides are identified by these steps, they can be assayed to determine their effect on *Phytophthora*. Importantly, the peptides identified in the examples were effective in inducing premature encystment of *Phytophthora* zoospores (see Appellants' Example 6 and Figs. 2 and 3). This is significant because premature encystment results in the disruption of the pathogenicity of the *Phytophthora* species. Thus, the peptides have an antifungal effect. In particular, the fraction of zoospores encysted by the Appellants' selected phage-bearing peptides was two to seven times greater than the fraction encysted by wild-type phage, as described in Example 6.

VI. GROUND'S OF REJECTION TO BE REVIEWED ON APPEAL

The only issue presented on appeal is whether the subject matter of claims 1-9 and 32-51 satisfy the requirements of 35 U.S.C. § 103(a). The grounds of rejection presented for review are as follows:

- A. Whether claims 1-4, 6-9, 32-34, 37-43, 45-47, and 49-51 are patentable under 35 U.S.C. § 103(a) over Gough et al. (J. Immunol. Methods 228 (1999) 97-108) in view of Kodadek (U.S. Pub. App. No. 2001/0029024) and Petrenko et al. (Protein Engineering 9(9) (1996) 797-801)
- B. Whether claims 44 and 49 are patentable under 35 U.S.C. § 103(a) over Gough et al. in view of Kodadek and Petrenko et al. as applied to claims 1-4, 6-9, 32-34, 37-43, 45-47, and 49-51, and further in view of Appellants' disclosure of known prior art.
- C. Whether claim 5 is patentable under 35 U.S.C. § 103(a) over Gough et al. in view of Kodadek and Petrenko et al. as applied to claims 1-4, 6-9,

32-34, 37-43, 45-47, and 49-51, and further in view of Smith et al.
(Methods Enzymol. 271 (1993) 228-257)

- D. Whether claims 35, 36, and 48 are patentable under 35 U.S.C. § 103(a) over Gough et al. in view of Kodadek and Petrenko et al. as applied to claims 1-4, 6-9, 32-34, 37-43, 45-47, and 49-51, and further in view of Qui et al. (U.S. Pat. No. 6,235,974)

VII. ARGUMENT

A. Rejection of claims 1-4, 6-9, 32-34, 37-43, 45-47, and 49-51 under 35 U.S.C. § 103(a) over Gough et al. in view of Kodadek and Petrenko et al.

For purposes of this ground of rejection, claims 1-4, 6-9, 32-34, 37-43, 45-47, and 49-51 do not stand or fall together. The claims have been divided into two groups: Group I (claims 1-4, 6-8, 32-34, 37-40, 45-47, and 49-51) and Group II (claims 9 and 41-43). The claims of each of Groups I and II are separately and independently patentable for the reasons described in Sections VII(A)(1)(a-d) and VII(A)(2)(a-d), *infra*.

1. Claims 1-4, 6-8, 32-34, 37-40, 45-47, and 49-51 (i.e., The Group I Claims)

Claim 1 is representative of the Group I claims. It is directed to a method for identification of **non-immunoglobulin** peptides having an affinity for the surface of a fungus. The method comprises (a) constructing a **library of peptides** by (i) preparing random oligonucleotides, (ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell, and (iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector; (b) contacting said vector expressing said peptide library with a target fungus and removing unbound vector; (c) eluting bound vector from said fungus; (d) amplifying said

bound vector; (e) sequencing the oligonucleotides contained in said eluted vector; (f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector; and (g) selecting the **non-immunoglobulin peptides** for which the amino acid sequence has been deduced.

a. Gough et al.

Gough et al. describe methods for the isolation of antibodies specific for surface-exposed epitopes on certain species of *Phytophthora* to be used for production of immunological probes and single-chain Fv (scFv) antibodies.²⁵ Gough et al.'s method involves adding germlings and soluble components thereof to maxisorb immunotubes, blocking, and incubating the maxisorb immunotubes with a **phage-displayed antibody library**.²⁶ The nonbound phage is removed, and the bound phage eluted and amplified in *E. coli*.²⁷ These steps are repeated, resulting in a discrete population of phage antibody fragments.²⁸ The diversity of the eluted antibodies is established by *Bst*NI fingerprinting, and DNA encoding for selected single-chain Fv antibodies is amplified by PCR, digested with restriction endonucleases, and ligated into a vector to produce scFv fusion proteins.²⁹ The scFv fusion proteins are then used to recognize external epitopes of *Phytophthora*.³⁰

Because many of the fungi used to assess the binding of the isolated single-chain Fv antibodies did not produce germlings that adhered to plastic surfaces, the antibodies isolated by Gough et al. had to be tested for their binding to mycelial homogenates.³¹ According to Gough et al., however, this assay could not be performed with phage-displayed single-chain Fv's because the phage-displayed form of the antibodies exhibited high background binding to the mycelial homogenates, which necessitated the production of soluble single-chain Fv's.³² Unfortunately, Gough et al. were also unable to produce detectable amounts of soluble single-chain Fv antibodies

²⁵ Gough et al. at page 98.

²⁶ *Id.* at page 99.

²⁷ *Id.*; see also pages 101-102.

²⁸ *Id.*

²⁹ Gough et al. at pages 98-99; see also pages 102-103.

³⁰ *Id.* at page 100; see also pages 103-104.

³¹ *Id.* at page 106.

³² *Id.*

from the DNA sequences encoding the selected antibodies.³³ Accordingly, the scFv genes had to be subcloned into an expression vector for the production of a fusion protein containing the single-chain Fv protein and a maltose binding protein (MBP).³⁴

While the methods of Gough et al. were generally effective in identifying antibodies that bind to the surface of *Phytophthora*, Gough et al. admit that their antibodies and others identified to date **have had no effect on *Phytophthora whatsoever***. Gough et al. still promise, however, that other antibodies to surface epitopes of *Phytophthora* having a pathogenic effect could still be identified:

The panning of whole pathogens might be expected to yield scFvs that bind to unmodified surface antigens that may be of importance in the infection process. However, preliminary assays, in which sporangia were mixed with soluble MBP-scFv fusion protein and then used to inoculate tomato leaf discs (Niderman et al., 1995), showed no detectable anti-fungal activity for any of the antibodies. Nevertheless, the isolation of other scFvs specifically directed against the native conformation of surface-accessible antigens may well provide new tools to probe and manipulate pathogenicity.³⁵

In contrast to the methods of Gough et al., claim 1 requires the use of a library of non-immunoglobulin peptides, not a library of scFv antibody fragments. Because Gough et al. are concerned with the isolation of antibodies for the surface-exposed epitopes on certain *Phytophthora* species to be used for immunological probes, they are using only single-chain Fv antibody fragments on phage in their disclosed phage display methods, and report no problems with the use of such antibody fragments for their objectives. Significantly, therefore, not only does Gough et al. fail to teach or suggest the use of vector-displayed random peptide libraries in their methods, they also fail to teach or suggest the selection of non-immunoglobulin peptides that bind epitopes on the surface of a fungus.³⁶ Furthermore, the substitution of random peptide libraries for antibody fragment libraries would be unproductive as Gough et al. seek to identify

³³ *Id.*

³⁴ *Id.*

³⁵ *Id.* at 107.

³⁶ See Appellants' Specification, page 9, lines 16-19 ("A "non-immunoglobulin peptide" means a peptide which is not an immunoglobulin, a recognized region of an immunoglobulin, or contains a region of an immunoglobulin. For example, a single chain variable region of an immunoglobulin would be excluded from this definition.").

antibodies which can be used in immunological methods, not mere non-immunoglobulin peptides.³⁷

In general, the single-chain Fv antibodies utilized in the methods of Gough et al. are far more complex than the simple peptides in the library of claim 1. Single-chain Fv antibodies such as those utilized in the methods of Gough et al. consist of three independent variable regions of amino acids that are constrained in some fashion (e.g., by folding) by the remaining scFv scaffold. Consequently, the three regions can interact with a target in a constrained manner that is complex and difficult to predict. The scFv scaffold itself may also interact with the target in some manner. Stated another way, the active binding portion of the antibody fragment may or may not work by itself upon subsequent isolation, and/or molecular structures and components other than the active binding portion may be responsible for binding epitopes or surface functions on the target independently or in conjunction with the active binding portion.

The random peptide libraries of claim 1 have far greater utility since they simply have some level of affinity to cell surface factors on the target fungus, without the additional ancillary protein sequences involved in the complex aspects of antibody structure and form. That is, the selected non-immunoglobulin peptides of Appellants' claimed invention can work outside of or independently from a phage-antibody framework to provide a more direct interaction with its targets.

A person of skill in the art must ignore the express teachings of Gough et al. to arrive at a non-immunoglobulin approach using simple peptide libraries. Most significantly, Gough et al.'s approach did not work, i.e., it "showed no detectable anti-fungal activity for any of the antibodies," and, at best, they hold out some vague hope for the future but this hope was limited to scFvs and NOT non-immunoglobulin peptides. Thus, a person of skill in the art would not and could not be motivated to substitute a library of peptides for antibodies in the methods of Gough et al. for the selection of non-immunoglobulin peptides.

The Office vaguely asserts that "the suggested teachings of Gough of non-macromolecular species (i.e., fragments) that retain the recognition characteristics

³⁷ In re Gordon, 733 F.2d 900, 221 USPQ2d 1125 (Fed. Cir. 1984); M.P.E.P. §2143.01. As stated by the Federal Circuit, if proposed a modification would render the prior art unsatisfactory for its intended purpose, then there is no suggestion or motivation to make the proposed modification.

of antibodies like small molecule peptides mimics [*sic*], would suggest the claimed peptide."³⁸ In fact, Gough et al. teaches and emphasizes the use of antibodies and only antibodies, not simply "species that retain the recognition characteristics of antibodies" as asserted by the Office. In sharp contrast, the Appellants' invention functions independently of immunological response (i.e., non-immunoglobulin) and is claimed as such.³⁹ Just because you happen to have a peptide that binds to an epitope does not mean that it is an "antibody mimic," as the Office is apparently asserting.

Finally, the Office notes that Gough et al. refer to similar strategies that have been applied to the selection of phage displayed peptides that bind to the surface of intact platelets.⁴⁰ This reference by Gough et al., however, implies that mere peptides would be inadequate to accomplish the clearly-stated objectives of Gough et al.

b. Kodadek

Kodadek describes methods of isolating small peptides that recognize **specific, known target peptides** (i.e., target peptides the identity and sequence of which are already known) for use in affinity purification. Kodadek's methods involve an elaborate genetic selection scheme to identify certain library encoded peptides having affinity to a single known target peptide (i.e., not a multitude of unknown epitopes such as those on the surface of a fungus).

Briefly, Kodadek's genetic selection scheme involves forming two compatible constructs, one encoding the known target peptide, and the other encoding a library of DNA fragments, and transforming them into *E. coli*.⁴¹ If a library encoded peptide is present in the library that associates with the target peptide, a complex between the library encoded peptide and the target peptide is formed.⁴² The complex blocks certain operator regions in *E. coli*, making it resistant to phage infection challenge.⁴³ Resistant colonies may then be selected, and the library encoded peptides that bind to the target peptide isolated.⁴⁴ As one example, Kodadek discloses utilizing as the target peptide a

³⁸ Office action dated July 25, 2005, at page 3.

³⁹ See Appellants' claim 1 and Appellants' Specification, page 9, lines 16-19.

⁴⁰ Office action dated July 25, 2005, at page 4.

⁴¹ Kodadek, page 4, paragraph [0042].

⁴² *Id.*; see also Kodadek, Figure 1.

⁴³ *Id.*

⁴⁴ *Id.*

13-residue sequence from the protease cleavage site of the human insulin-like growth factor I (IGF-I).⁴⁵

In contrast to the Appellants' claimed invention, Kodadek is concerned with the selection of library encoded peptides having affinity to a single, specific, known target peptide, not a surface with a multitude of unknown epitopes such as the surface of a fungus. Kodadek is not contacting his library encoded peptides with anything other than a provided target peptide (e.g., the protease cleavage site of the human insulin-like growth factor I) to identify binding partners to that particular target.

In essence, Kodadek is describing a prokaryotic analog of a conventional two-hybrid system.⁴⁶ Two-hybrid systems, in general, are assays for the detection of peptide-peptide interactions and the identification of genes encoding interactive proteins. As demonstrated by a number of references cited by Kodadek, the use of two-hybrid systems for such purposes is well-known in the art.⁴⁷ Like Kodadek, the common two-hybrid system typically involves the interaction of peptides in a peptide library with a target peptide. Generally speaking, however, the two-hybrid system is a much more indirect assay as compared to that of Gough et al. Other than the mere fact that peptides in a peptide library happen to be binding to other peptides (e.g., peptide epitopes), there is no apparent reason why one of skill in the art would be motivated to substitute a library of peptides into the methods of Gough et al. based on Kodadek's disclosure, or any other reference that merely describes the interaction of known peptides with a peptide library for that matter.

Furthermore, Kodadek actually **teaches away** from the use of phage display methods to identify library encoded peptides. Specifically, Kodadek suggests the superiority of his elaborate genetic selection scheme, where other methods have failed. In so doing, Kodadek notes that both **random peptides** (used in the present invention) and antibodies (used in Gough et al.) are **inadequate** for his purpose. As such, Kodadek and Gough et al. represent mutually exclusive domains, and, therefore, any suggestion of substitution of the peptides of Kodadek into the methods of Gough et al.

⁴⁵ *Id.* at page 4, paragraph [0039].

⁴⁶ See, e.g., Kodadek, page 4, paragraphs [0037]-[0040].

⁴⁷ See, e.g., Kodadek, page 4, paragraph [0038], and the list of references provided by Kodadek on pages 18-21, paragraphs [0167]-[0321].

would not be feasible. Thus, one skilled in the art would not and could not be motivated to substitute the highly specialized method of Kodadek into the method of Gough et al. without violating the objective of Gough et al. and rendering it unsatisfactory for its intended purpose.⁴⁸

The Office has asserted that, by describing the disadvantages in the use of antibodies, Kodadek provided the motivation to substitute peptides into the methods of Gough et al. The Office's assertions apparently rest upon Kodadek's disclosure that "advances in the construction of single chain antibody libraries [scFv's] on phage promise to speed up this process."⁴⁹ However, in light of the fact that Kodadek discloses various drawbacks to the use of antibodies in binding studies, the quoted language is nothing more than a suggestion that the disadvantages of antibody usage may be minimized by phage display methodology.

More importantly, Kodadek, in addition to describing the disadvantages of antibodies, also discloses similar disadvantages of peptides, stating that "[u]nfortunately, peptides, or peptide epitopes in proteins, are difficult targets for molecular recognition in aqueous solution,"⁵⁰ and that early efforts by Kodadek and co-workers to isolate small peptides using phage display methods "failed completely."⁵¹

Unlike the case for antibodies, Kodadek is devoid of any suggestion that the disadvantages of peptide usage disclosed therein are minimized by any means. Instead, after encountering first-hand the limitation and/or failure of antibodies and phage display, Kodadek resorted to his genetic selection scheme described above to identify certain library encoded peptides having affinity to a given target peptide. Kodadek further describes that, in some cases, even the genetically selected library encoded peptides may not possess the desired affinity for the target.⁵² In this event, Kodadek describes that conventional phage display methods may be modified by

⁴⁸ See *supra*, note 37.

⁴⁹ Kodadek, page 1, paragraph [0009] (internal citations omitted).

⁵⁰ *Id.* at paragraph [0006].

⁵¹ Kodadek, page 4, paragraph [0038]. Appellants respectfully submit that it is the Office, not the Appellants, which has taken Kodadek's disclosure out of context on this point. (See Office action dated July 25, 2005, at pages 6-7). Clearly Kodadek is referring to the failure of phage display as supporting the biases against the use of peptides.

⁵² *Id.* at pages 13-14, paragraphs [0125]-[0134].

attaching the genetically selected library encoded peptide to the end of a standard phage displayed peptide library to form a "pincer."⁵³ The affinity of the genetically selected library encoded peptide arm is improved by the addition of the phage displayed peptide library because the library encoded peptide arm and the phage displayed random peptide library arm wrap around the target peptide.⁵⁴ Kodadek's specialized "pincer" approach thus facilitates identification of peptide-target interaction where the original peptide-epitope interaction (i.e., the library encoded peptide-known target interaction in the genetic selection scheme) is insufficient for stable interaction.⁵⁵

Instead of providing motivation, a close reading of Kodadek clearly indicates that one skilled in the art would actually be guided away from combining the disclosures of Gough et al. and Kodadek. Keeping this standard in mind, it is significant that Kodadek refers to the futile attempts to identify peptide complexes using phage display that, in Kodadek's words, not only failed but "failed completely." Kodadek then goes on to describe his genetic selection scheme designed to be an improved method, in and of itself, to overcome past failures in identifying peptide complexes. It is only after particular, weakly-binding library encoded peptides that bind to the known target peptide are identified by the genetic selection scheme (i.e., on the basis of affinity) that Kodadek coupled them with conventional phage display methods to form a pincer. Thus Kodadek clearly implies (and in some respects states outright) that conventional phage display methods, standing on their own, would not work. Why else would Kodadek go to all the trouble of devising the genetic selection scheme if random peptide phage display alone would be effective?

c. Petrenko et al.

Petrenko et al. describe methods of forming phage-displayed "landscape libraries" having complex surface functions that would be useful, e.g., in nanotechnology applications. According to Petrenko et al., the complex surface functions of phage clones depend on interactions between neighboring groups of display peptides and wild-type peptides.⁵⁶ The emergent properties of the phage surface inhere (i.e., are

⁵³ *Id.* at page 14, paragraph [0132].

⁵⁴ *Id.* at paragraphs [0132]-[0133]; *see also* Kodadek, Figure 7.

⁵⁵ *Id.*

⁵⁶ Petrenko et al. at page 797.

intrinsic) in the entire surface of the phage, not in the display peptides themselves.⁵⁷ Stated another way, Petrenko et al. describe modifications to phage such that the phage will display "global properties" across the entire surface of the phage, not only mere localized properties of the particular displayed peptides. As an example, Petrenko et al. suggest as desirable a phage with a high affinity for a metal ion that displays metal complexed on the surface in a specific repeating geometry.⁵⁸ Petrenko et al. also specifically disclose experiments where phage clones were selected for the "global property" of chloroform resistance.⁵⁹ Petrenko et al. also describe panning phage displayed peptides against a particular known target material. Such targets included dioxin in one experiment and the lectin concanavalin A in another experiment. In both cases, the phage displayed library of peptides was panned against a **single known target** (i.e., not a multitude of unknown targets such as those on the surface of a fungus).

The lack of teaching, suggestion, or motivation in Gough et al. and Kodadek is not remedied by the disclosure of Petrenko et al. Petrenko et al. describe panning phage displayed peptides against, like Kodadek, a **single known target** seeking to identify phage clones that exhibit "global properties" across the entire phage surface (e.g., chloroform resistance), irrespective of the particular peptides of the library. The "global functions" described in Petrenko et al. were a means to select phage clones that were sensitive to chloroform and to demonstrate that chloroform resistance of the phage depended on the global surface properties of the phage. For example, in Petrenko et al., the mosaic phage was up to 10,000 times more sensitive to chloroform than the corresponding non-mosaic phage.⁶⁰

This is in sharp contrast to the methods of Gough et al., where the target was a multitude of unknown surface epitopes presented on the surface of *Phytophthora*, and the authors were seeking to identify specific antibodies that bind to the surface of *Phytophthora*. Therefore, one skilled in the art would not and could not be motivated to modify the methods of Gough et al. according to the methods described in Petrenko et

⁵⁷ *Id.*

⁵⁸ *Id.* at 801.

⁵⁹ *Id.* at 789-799.

⁶⁰ Petrenko et al. at page 799.

al. as such a modification would fail to achieve the clearly-stated objectives of each reference.⁶¹

Moreover, at no point in Petrenko et al. and/or Gough et al. is there any discussion, disclosure, or inference about how the localized properties of phage-peptide interactions provide an advantage over phage-antibody fragments for the isolation of antibodies. It is not enough that the peptide libraries, or specifically Petrenko et al.'s f8-1 peptide library, could be theoretically substituted into the methods of Gough et al.⁶²

In contrast to the focus and methods of Petrenko et al., claim 1 is directed to the identification of peptides displayed on the surface of a vector that have a binding affinity for epitopes displayed on the surface of *Phytophthora*. This goal does not necessarily implicate "global functions" that inhere in the entire surface of phage-peptide. In fact, claim 1 does not even require that the peptide library be expressed on phage. Rather, the peptide library is expressed on a vector, and any vector capable of expressing the peptides of the peptide library may be used.⁶³ Contrary to the Office's assertion otherwise, the mosaic nature of phage-displayed peptides in Petrenko et al. provides neither suggestion nor motivation to substitute peptides for antibody fragments in the method of Gough et al. in order to identify non-immunoglobulin peptides with affinity for surface epitopes of *Phytophthora*.

Finally, the Office asserts that Petrenko et al. extol the "global functions" that inhere in the entire surface landscape of phage-peptide as motivation to substitute peptides for antibody fragments in the method of Gough et al. As stated above, however, the objectives of Petrenko et al. (global functions) and Gough et al. (antibodies) are far too disparate for one skilled in the art to make such a substitution, particularly since such a substitution would render the prior art being modified unsatisfactory for its intended purpose.⁶⁴

⁶¹ See *supra*, note 37.

⁶² *In re Mills*, 916 F.2d 680, 16 USPQ2d 1430 (Fed. Cir. 1990); M.P.E.P. §2143.01. The mere fact that references can be combined or modified does not render the resultant combination obvious unless the prior art also suggests the desirability of the combination.

⁶³ See Appellants' Specification, page 11, lines 3-19.

⁶⁴ See *supra*, note 37.

d. The Prior Art Provides No Reasonable Expectation of Success

Collectively, and individually, Gough et al., Kodadek and Petrenko et al. fail to disclose a method for the identification of a peptide, immunoglobulin or otherwise, having anti-fungal properties. Gough et al. merely identified immunoglobulin peptides that bind to the surface of *Phytophthora*; Gough et al. **failed** to demonstrate that their scFvs had any antifungal effect and merely expressed some vague hope that **scFvs** may **one day** "provide new tools to probe and manipulate pathogenicity."⁶⁵ Kodadek was not concerned with the identification of peptides having antifungal properties. Instead, Kodadek was concerned with two-hybrid methods and modifications thereto for isolating small peptides that recognize specific, known target peptides for use in affinity purification; significantly, however, Kodadek developed this approach because **the random peptide approach** (used in the present invention) and antibodies (used in Gough et al.) **were inadequate** for his purpose. Petrenko et al. were concerned with forming phage-displayed "landscape libraries" of general applicability and did not suggest any means for identifying antifungal peptides.

Against this backdrop, claim 1 defines a method which has been successfully used to identify non-immunoglobulin peptides which has been demonstrated to yield peptides having antifungal properties. According to the Office, this approach was obvious despite the fact that Gough et al., the only reference cited by the Office relating to antifungal peptides, **failed to identify any peptides having antifungal properties** and Kodadek said the random peptide approach **failed completely**.⁶⁶ Somehow, the Office has concluded a person of ordinary skill would have been led to adopt the method of claim 1 with an expectation of success despite the fact that not one of the three references cited by the Office successfully accomplished this and one of them said that prior attempts to use Applicants' approach failed completely.⁶⁷ Simply stated, the Office's rejection of claim 1 is nothing more and nothing less than an impermissible hindsight rejection, using Appellants' disclosure as a template.⁶⁸

⁶⁵ Gough et al. at page 107.

⁶⁶ Kodadek, page 4, paragraph [0038].

⁶⁷ *Amgen, Inc. v. Chugai Pharmaceutical Co.*, 927 F.2d 1200, 1207-8, 18 USPQ2d 1016, 1022-23 (Fed. Cir. 1991) *cert. denied*, 502 U.S. 856 (1991).

⁶⁸ *M.P.E.P.* §2141; *U.S. v. Adams*, 383 U.S. 39 (1965); *Panduit Corp. v. Dennison Mfg. Co.*, 774 F.2d 1082, 227 USPQ 337 (Fed. Cir. 1985), *vacated and remanded on other grounds*, 475 U.S. 809, 106 S.Ct.

2. Claims 9 and 41-43 (The Group II Claims)

Claim 9 is representative of the Group II claims. It depends from claim 1 (or claim 48) and additionally requires that each of the peptides be the same length, the length being 6 to 15 amino acids.⁶⁹

a. **Gough et al.**

As discussed above, Gough et al. describe methods for the isolation of antibodies specific for surface-exposed epitopes on certain species of *Phytophthora* to be used for production of immunological probes and single-chain Fv (scFv) antibodies.⁷⁰ In contrast to the methods of Gough et al., claim 9 requires the use of peptides that are the same length, the length being 6 to 15 amino acids, not scFv antibody fragments.

The single-chain Fv antibodies utilized in the methods of Gough et al. are far more complex than the simple, 6- to 15-mer random peptides required by claim 9. While the Office cites no authority regarding the molecular weight of scFv antibodies, it is the Appellants' understanding that such scFv antibodies generally have a molecular weight of at least about 24,000, with 29,000 to 30,000 being typical. Based on a molecular weight of 24,000 and using an average molecular weight of 137 for the 20 possible amino acids, Gough et al.'s antibody fragments would be about 175 amino acids in length; thus, Gough et al.'s antibody fragments are, at a minimum, 12 times longer than the 6- to 15-mer peptides required by claim 9. In addition, Gough et al.'s single-chain Fv antibodies include ancillary protein sequences that are involved in antibody structure and form, and may not work outside or independent of the complex phage-antibody framework.⁷¹ Thus, not only do Gough et al. fail to teach or suggest the use of peptides in their methods, they also fail to teach or suggest peptides having the same length, the length being 6 to 15 amino acids.

1578 (1986), *adhered to on remand*, 810 F.2d 1561, 1 USPQ2d 1593 (Fed. Cir. 1987); W.L. Gore & Assoc., Inc. v. Garlock, Inc., 721 F.2d 1540, 220 U.S.P.Q. 303, 313 (Fed. Cir. 1983), *cert. denied*, 469 U.S. 851 (1984).

⁶⁹ The Group II claims are claims 9 and 41-43. Claim 41 is comparable to claim 9 except that it requires the peptides to be 8 amino acids in length. Claim 42 requires the peptide library to be the f8-1 peptide library. Claim 43 requires the peptides to be of the same length, the length being 15 amino acids. As described in Appellants' Specification page 11, lines 3-19, the f8-1 peptide library includes random peptides that are 8 amino acids in length and the f88-4 peptide library includes random peptides that are 15 amino acids in length.

⁷⁰ See *supra* Section VII(A)(1)(a).

⁷¹ See *supra* Section VII(A)(1)(a).

A person of skill in the art must ignore the express teachings of Gough et al. to arrive at peptides having the same length, the length being 6 to 15 amino acids. Most significantly, Gough et al.'s approach "showed no detectable antifungal activity for any of the antibodies," and, at best, they hold out a vague hope for the future limited only to scFv antibodies and not peptides of a specific length.⁷²

b. Kodadek

As discussed in detail above, Kodadek is concerned with the selection of library encoded peptides having an affinity to a single, specific, known target peptide, not a surface with a multitude of unknown epitopes such as the surface of a fungus. To accomplish his goals, Kodadek describes modifications to a conventional two-hybrid system. In so doing, Kodadek notes that both **random peptides** (e.g., 6 to 15-mer peptides required by claim 9) and antibodies (used in Gough et al.) are **inadequate** for his purpose. Most significantly, at the time of the present invention Kodadek had already stated that phage display methods were not only ineffective in identifying small peptides, they were a **complete failure**.⁷³ Thus, Kodadek **teaches away** from the use of phage display methods to identify library encoded peptides, regardless of length.

c. Petrenko et al.

Petrenko et al., like Kodadek, describe panning phage-displayed peptides against a single known target seeking to identify phage clones that exhibit "global properties" across the entire phage surface. That is, Petrenko et al. describe modifications to phage such that the phage will display "global properties" across the entire surface of phage, not only mere localized properties of the particular displayed peptides.⁷⁴ This is in sharp contrast to the methods of Gough et al., where the target was a multitude of unknown surface epitopes presented on the surface of *Phytophthora* and the authors were seeking to identify specific antibodies that bind to the surface of *Phytophthora*.

⁷² *Id.* See also Gough et al. at page 107.

⁷³ See *supra* Section VII(A)(1)(b). See also Kodadek, page 4, paragraph [0038].

⁷⁴ See *supra* Section VII(A)(1)(c). See also Petrenko et al. at page 797.

d. The Prior Art Provides No Reasonable Expectation of Success

At the time of Appellants' invention, Petrenko et al.'s peptide libraries were known in the art, and Gough et al. still selected a phage-antibody library of scFv fragments. Incredibly, the Office has nonetheless concluded that Petrenko et al.'s phage-displayed peptides could be substituted into the methods of Gough et al. The Office makes this assertion despite the fact that Gough et al.'s method "showed no detectable antifungal activity for any of the antibodies" and Kodadek said it would not work. There is simply **no reason** to believe that the substitution of smaller peptides such as those having a length of 6 to 15 amino acids would even work, let alone provide an improvement over the larger scFv antibodies of Gough et al.

B. Rejection of claims 44 and 49 under 35 U.S.C. § 103(a) over Gough et al. in view of Kodadek and Petrenko et al., and further in view of Appellants' disclosure of known prior art

1. Claims 44 and 49

Claim 44 is representative of this group of claims.⁷⁵ It depends from claims 1 or 48 and additionally recites that the library of peptides is an f88-4 peptide library. Independent claim 49 is similar to claim 1 discussed above and recites that the library of peptides is (1) an f8-1 peptide library, wherein each peptide of the f8-1 peptide library has a length of 8 amino acids, or (2) an f88-4 peptide library wherein each peptide of the f88-4 peptide library has a length of 15 amino acids.

Gough et al., Kodadek, and Petrenko et al. are discussed in detail above.

At the time of Appellants' invention, random peptide libraries in general were known in the art, and included such random peptide libraries as the f8-1 and the f88-4 phage-displayed peptide libraries. Accordingly, Appellants' specification describes

⁷⁵ Claim 49 is comparable to claim 44 except that it is an independent claim and recites that the library of peptides is (1) an f8-1 peptide library, wherein each peptide of the f8-1 peptide library has a length of 8 amino acids, or (2) an f88-4 peptide library wherein each peptide of the f88-4 peptide library has a length of 15 amino acids. Notably, claim 49 was rejected by the Office according to ground A above (i.e., Gough et al. in view of Kodadek and Petrenko et al.) and also according to ground B (i.e., Gough et al. in view of Kodadek and Petrenko et al., and further in view of the Appellants' disclosure of known prior art). See Office action dated February 9, 2006, at page 4. Accordingly, Appellants have included claim 49 in their arguments for patentability directed to each of these grounds of rejection.

some of the features of the f8-1 and the f88-4 phage-displayed peptide libraries that may be used in the Appellants' claimed invention and provides citations for the relevant art describing **methods for the production** of these phage-displayed peptide libraries.⁷⁶

None of the references cited by the Appellants describe the use of the f8-1 and/or the f88-4 phage-displayed peptide libraries in connection with *Phytophthora* species, nor do they suggest that such uses could be carried out. Thus, while the f8-1 and the f88-4 phage-displayed peptide libraries and methods for their production were known, it was nonetheless nonobvious to use such phage-displayed peptide libraries to pan against surface exposed epitopes on *Phytophthora* species. In fact, claim 44 does not even require that the peptide library be expressed on phage. Rather, the peptide library is expressed on a vector, and any vector capable of expressing the peptides of the peptide library may be used.⁷⁷ Contrary to the Office's assertion otherwise, the disclosure of the features of the f8-1 and the f88-4 phage-displayed peptide libraries and references describing methods for their production provide neither suggestion nor motivation to substitute the f8-1 or the f88-4 peptide libraries for antibody fragments in the method of Gough et al. in order to identify non-immunoglobulin peptides with affinity for surface epitopes of *Phytophthora*.

The references cited by Appellants as describing features and methods for the production of the f8-1 and the f88-4 phage-displayed peptide libraries pre-date Gough et al. by at least three years, yet Gough et al. still selected a phage-**antibody** library of scFv fragments. The Office has nonetheless concluded that the f8-1 and/or the f88-4 phage-displayed peptide libraries could be substituted into the methods of Gough et al. The Office makes this assertion despite the respective disclosures of Gough et al. and Kodadek discussed above; namely, that Gough et al.'s method showed no detectable antifungal activity for any of the antibodies and Kodadek said it would not work. There is simply **no reason** to believe that the substitution of the f8-1 and/or the f88-4 peptide libraries would even work, let alone provide an improvement over the larger scFv antibodies of Gough et al.

⁷⁶ See Appellants' Specification, page 11, line 20 to page 12, line 2.

⁷⁷ See Appellants' Specification, page 11, lines 3-19.

As a result, claim 44 is nonobvious and patentable over Gough et al. in view of Kodadek and Petrenko et al., and further in view of the Appellants' disclosure of known prior art.

C. Rejection of claim 5 under 35 U.S.C. § 103(a) over Gough et al. in view of Kodadek and Petrenko et al., and further in view of Smith et al.

1. Claim 5

Claim 5 depends from claim 1 discussed above, and recites that the sequence of the random oligonucleotide is GCA GNN (NNN)₇ or SEQ ID NO: 1.

Gough et al., Kodadek, and Petrenko et al. are discussed in detail above.

Smith et al. is a review article discussing conventional libraries of peptides and phage-displayed proteins and methods for their production. Smith et al. discuss the use of degenerate oligonucleotides and their use in the production of peptide libraries having synthetic degenerate (i.e., random) oligonucleotides as the insert.⁷⁸ This feature is the nature of the "random" peptide library.

Like the f8-1 and the f88-4 phage-displayed peptide libraries, random oligonucleotides and their use in peptide libraries is known in the art. Smith et al., however, provide neither suggestion nor motivation to utilize degenerate oligonucleotides in the methods of Gough et al. Further, there is no reason to believe that the substitution of random peptide libraries formed using degenerate oligonucleotides would even work, let alone provide an improvement over antibody fragments, given the respective disclosures of Gough et al., Kodadek, Petrenko et al., and Smith et al. discussed above.

As a result, claim 5 is nonobvious and patentable over Gough et al. in view of Kodadek and Petrenko et al., and further in view of Smith et al.

⁷⁸ See Smith et al. at pages 243-245.

D. Rejection of claims 35, 36, and 48 under 35 U.S.C. § 103(a) over Gough et al. in view of Kodadek and Petrenko et al., and further in view of Qui et al.

1. Claims 35, 36, and 48

Claim 48 is representative of this group of claims.⁷⁹ It is similar to claim 1 discussed above, and recites that the target fungus is selected from the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, and *Phytophthora parasitica*.

Gough et al., Kodadek, and Petrenko et al. are discussed in detail above.

Qui et al. is directed to methods for imparting pathogen resistance to plants by applying a hypersensitive response elicitor polypeptide isolated from its corresponding organism to a plant seed. According to Qui et al., the elicitors are polypeptides or proteins that are able to elicit local necrosis (i.e., a hypersensitive response) in plant tissue contacted by the elicitor.⁸⁰ The elicitor-mediated hypersensitive response is a widely distributed pathogen defense mechanism known to occur across a wide variety of plant species in response to bacterial and fungal pathogens.⁸¹ Accordingly, Qui et al. describe that their elicitor polypeptides are “derived from a wide variety of fungal and bacterial pathogens.”⁸² As examples of bacterial sources for their elicitor polypeptides, Qui et al. mention *Erwinia*, *Pseudomonas*, and *Xanthomonas* species, and as examples of fungal sources for their elicitor polypeptides, Qui et al. mention *Phytophthora*.⁸³ *Phytophthora parasitica*, *Phytophthora cryptogea*, *Phytophthora cinnamomi*, *Phytophthora capsici*, *Phytophthora megasperma*, and *Phytophthora citrophthora* are listed as suitable source materials for the elicitor polypeptides.⁸⁴

There are a number of *Phytophthora* species known in the art, some of which are cited in the Appellants’ specification and/or the disclosure of Qui et al., others which are

⁷⁹ Claim 35 is comparable to claim 48 except that it depends from claim 1 discussed above. Claim 36 is comparable to claim 35 except that it recites that the target fungus is *Phytophthora sojae* or *Phytophthora capsici*.

⁸⁰ See Qui et al. at col. 7, lines 5-10.

⁸¹ *Id.* at col. 1, line 18 to col. 6, line 6.

⁸² *Id.* at col. 7, lines 6-9.

⁸³ *Id.* at col. 7 lines 11-19.

⁸⁴ *Id.* at col. 7, lines 20-23.

not. Other than naming three of the five *Phytophthora* species recited in Appellants' claim 48, the Qui et al. reference is non-analogous to the Appellants' invention. Rather than choosing to cite an index of all formal names in the Kingdom Fungi pertaining to *Phytophthora*, the Office apparently chose Qui et al.

Qui et al. do not suggest that any of the numerous source fungi for hypersensitive response elicitor polypeptides would be desirable in the methods of Gough et al. The methods of Gough et al. and Qui et al. are far too disparate for one of skill in the art to combine. In other words, while Qui et al. recited several exemplary *Phytophthora* species as sources for their elicitor polypeptides, some of which were included in the Appellants' claim 48, this disclosure would not motivate one skilled in the art to substitute various *Phytophthora* species in the methods of Gough et al.

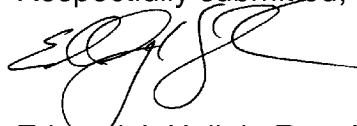
As a result, claim 48 is nonobvious and patentable over Gough et al. in view of Kodadek and Petrenko et al., and further in view of Qui et al.

E. Conclusion

A *prima facie* case of obviousness has not been established pursuant to 35 U.S.C. § 103(a) based on the combined references of Gough et al., Kodadek, and Petrenko et al. It has not been shown that the cited references would have motivated a person of ordinary skill in the art to make the Appellants' invention, would have provided a reasonable expectation of success, or when considered as a whole, would have suggested all of the requirements of the claimed invention. For these reasons, and for those more fully stated above, Appellants respectfully request the rejections be reversed and claims 1-9 and 32-51 be allowed.

The Commissioner is hereby authorized to charge any additional fees which may be required to Deposit Account No. 19-1345.

Respectfully submitted,

A handwritten signature in black ink, appearing to read 'EJH', with a long horizontal flourish extending to the right.

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EJH/BJS/clh

VIII. CLAIMS APPENDIX

1. (Previously presented) A method for identification of non-immunoglobulin peptides having an affinity for the surface of a fungus comprising:

- (a) constructing a library of peptides by,
 - (i) preparing random oligonucleotides;
 - (ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell;
 - (iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector;
- (b) contacting said vector expressing said peptide library with a target fungus and removing unbound vector;
- (c) eluting bound vector from said fungus;
- (d) amplifying said bound vector;
- (e) sequencing the oligonucleotides contained in said eluted vector;
- (f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector; and
- (g) selecting the non-immunoglobulin peptides for which the amino acid sequence has been deduced.

2. (Previously presented) The method of any one of claims 1, 48, or 49 further comprising repeating steps (b) through (d) at least once.

3. (Previously presented) The method of any one of claims 1, 48, or 49, wherein said vector is a fusion phage vector.

4. (Previously presented) The method of any one of claims 1, 48, or 49, wherein said vector is a fusion phage vector selected from the group consisting of type 8, type 88, type 8+8, type 3, type 33, type 3+3, type 6, type 66, type 6+6, phage T7 and phage 8.

5. (Previously presented) The method of any one of claims 1 or 48, wherein the sequence of said random oligonucleotide is GCA GNN (NNN)₇ or SEQ ID NO: 1.

6. (Previously presented) The method of any one of claims 1, 48, or 49, wherein said peptide is expressed as part of a coat protein of said vector.

7. (Original) The method of claim 6, wherein said coat protein is a pIII or a pVIII coat protein.

8. (Previously presented) The method of any one of claims 1, 48, or 49, further comprising determining the binding affinity of said peptides to said target fungus.

9. (Previously presented) The method of any one of claims 1 or 48, wherein each of said peptides are of the same length, the length being 6 to 15 amino acids.

Claims 10 - 31. (Canceled)

32. (Previously presented) The method of any one of claims 1 or 49 wherein the target fungus is a plant pathogenic fungus.

33. (Previously presented) The method of any one of claims 1 or 49 wherein the target fungus is a member of genus *Phytophthora*.

34. (Previously presented) The method of any one of claims 1 or 49 wherein the target fungus is selected from the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora cactorum*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, *Phytophthora infestans*, and *Phytophthora parasitica*.

35. (Previously presented) The method of any one of claims 1 or 49 wherein the target fungus is selected from the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, and *Phytophthora parasitica*.

36. (Previously presented) The method of any one of claims 1 or 49 wherein the target fungus is *Phytophthora sojae* or *Phytophthora capsici*.

37. (Previously presented) The method of any one of claims 1, 48, or 49 wherein the vector expressing the peptide library is contacted with the target fungus at different life stages of the target fungus.

38. (Previously presented) The method of any one of claims 1, 48, or 49 wherein the vector expressing the peptide library is contacted with the target fungus at oospore life stage or chlamydospore life stage.

39. (Previously presented) The method of any one of claims 1, 48, or 49 wherein the vector expressing the peptide library is contacted with the target fungus at zoospore life stage.

40. (Previously presented) The method of any one of claims 1, 48, or 49 wherein the vector expressing the peptide library is contacted with the target fungus at germling life stage.

41. (Previously presented) The method of any one of claims 1 or 48 wherein each of said peptides are of a same length, the length being 8 amino acids.

42. (Previously presented) The method of any one of claims 1 or 48 wherein the peptide library is an f8-1 peptide library.

43. (Previously presented) The method of any one of claims 1 or 48 wherein each of said peptides are of a same length, the length being 15 amino acids.

44. (Previously presented) The method of any one of claims 1 or 48 wherein the peptide library is an f88-4 peptide library.

45. (Previously presented) The method of any one of claims 1, 48, or 49, further comprising repeating steps (b) through (d) at least twice.

46. (Previously presented) The method of any one of claims 1, 48, or 49, further comprising repeating steps (b) through (d) at least three times.

47. (Previously presented) The method of any one of claims 1, 48, or 49 wherein the bound vector is amplified in an *E. coli*.

48. (Previously presented) A method for identification of non-immunoglobulin peptides having an affinity for the surface of a fungus comprising:

(a) constructing a library of peptides by,

(i) preparing random oligonucleotides;

(ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell;

(iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector;

(b) contacting said vector expressing said peptide library with a target fungus and removing unbound vector, wherein the target fungus is selected from the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, and *Phytophthora parasitica*;

(c) eluting bound vector from said fungus;

(d) amplifying said bound vector;

(e) sequencing the oligonucleotides contained in said eluted vector;

(f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector; and

(g) selecting the non-immunoglobulin peptides for which the amino acid sequence has been deduced.

49. (Previously presented) A method for identification of non-immunoglobulin peptides having an affinity for the surface of a fungus comprising:

(a) constructing a library of peptides by,

(i) preparing random oligonucleotides;

(ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell;

(iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector;

wherein the library of peptides is (1) an f8-1 peptide library, wherein each peptide of the f8-1 peptide library has a length of 8 amino acids or (2) an f88-4 peptide library, wherein each peptide of the f88-4 peptide library has a length of 15 amino acids;

(b) contacting said vector expressing said peptide library with a target fungus and removing unbound vector;

(c) eluting bound vector from said fungus;

(d) amplifying said bound vector;

(e) sequencing the oligonucleotides contained in said eluted vector;

(f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector; and

(g) selecting the non-immunoglobulin peptides for which the amino acid sequence has been deduced.

50. (Previously presented) The method of claim 49 wherein the library of peptides is a f8-1 peptide library, wherein each peptide of the f8-1 peptide library has a length of 8 amino acids.

51. (Previously presented) The method of claim 49 wherein the library of peptides is a f88-4 peptide library, wherein each peptide of the f88-4 peptide library has a length of 15 amino acids.

XI. EVIDENCE APPENDIX

None.

X. **RELATED PROCEEDINGS APPENDIX**

None.